SEQUENCE LISTING

<110> Davis, S. Christopher
Grate, John H.
Gray, David R.
Gruber, John M.
Huisman, Gjalt W.
Ma, Steven K.
Newman, Lisa M. Sheldon, Roger
Wang, Li A.

<120> Enzymatic Processes for the Production
of 4-Substituted 3-Hydroxybutyric Acid Derivatives and
Vicinal Cyano, Hydroxy-substituted Carboxylic Acid Esters

<130> 0339.310US

<150> US 10/639,159
<151> 2003-08-11

<150> US 60/402,436
<151> 2002-08-09

<160> 126

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KRED CR2-5

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<222> (1)...(852)

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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
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cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
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aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
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aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat ata ata gta gat gga gga tat aca tta ccc taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
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<210> 2
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<213> Candida magnoliae

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            20   25   30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35   40   45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50   55   60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65   70   75   80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85   90   95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100   105   110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115   120   125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130   135   140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145   150   155   160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165   170   175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180   185   190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195   200   205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210   215   220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225   230   235   240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245   250   255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260   265   270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275   280

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 1               5                  10                  15

cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat     240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca     288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat     336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gta gca gca aat gca gga ata ccc tgg aca aag gga gca tat ata     384
Ile Val Ala Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta     432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa     480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc     528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat     576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag     624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat     672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
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aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat ata ata gta gat gga gga tat aca tta ccc taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
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<213> Candida magnoliae

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            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Ala Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
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Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
         35                  40                  45

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
     50                  55                  60

aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc      528
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Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat ata ata gta gat gga gga tat aca tta ccc taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
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<210> 6
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<213> Candida magnoliae

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            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
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145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
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 1               5                  10                  15

cat aca aag aat gag agc tta caa gta tta gat tta ttt aag tta aat       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

gga aaa gta gca agc ata aca gga agc agc agc gga ata gga tat gca      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

tta gca gag gct ttt gca caa gtc gga gca gat gta gca ata tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aat agc cat gat gca aca gga aaa gca gag gca tta gca aag aag tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

gga gta aag gta aag gca tat aaa gca aat gta agc agc agc gat gca      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtc aag caa aca ata gag caa caa ata aag gat ttt gga cat tta gat      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
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```
            100                 105                 110

ata gta gta gca aat gca gga ata ccc tgg aca aag gga gca tat ata      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat caa gat gat gac aag cat ttt gac caa gta gta gat gta gac tta      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aag gga gta gga tac gta gca aag cat gca gga agg cat ttt agg gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

agg ttt gag aaa gag gga aaa aag gga gca tta gta ttt aca gca agc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg agc gga cat ata gta aat gtc ccc caa ttc caa gca aca tat aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gca gca aag gca gga gta agg cat ttt gca aag agc tta gca gtc gag      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gca ccc ttt gca agg gta aat agc gta agc ccc gga tat ata aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

aca gag ata agc gat ttc gtc ccc caa gag aca caa aat aag tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtc ccc tta gga agg gga gga gag aca gca gag tta gta gga      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gca tat tta ttc tta gca agc gat gca gga agc tat gca aca gga aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat ata ata gta gat gga gga tat act tta ccc taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
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<210> 8
<211> 283
<212> PRT
<213> Candida magnoliae

<400> 8

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            20                  25                  30
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Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
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<220>
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<223> Glucose dehydrogenase S06-3

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 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca       96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
             20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta      144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
         35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga      192
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Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
     50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att      240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                 85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat      624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa                                             786
Gln Ala Gly Arg Gly  *
            260
```

<210> 10

<211> 261
<212> PRT
<213> Bacillus sp.

<400> 10
```
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
```

<210> 11
<211> 786
<212> DNA
<213> Bacillus sp.

<220>
<221> CDS
<222> (1)...(786)
<223> Glucose dehydrogenase M02-6

<400> 11
```
atg tat aaa gat tta gaa gga aaa gta gtt gtc ata aca ggt tca tct       48
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1               5                  10                  15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct       96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
```

```
                20                  25                  30

aaa gta gtt gtg aat tat cgt tcg aaa gaa gaa gaa gct aac agc gtt      144
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
         35                  40                  45

tta gaa gaa att aaa aaa gtc ggc gga gag gca att gcg gtt aaa ggt      192
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
     50                  55                  60

gac gta aca gtt gag tct gac gtg atc aat tta gtt caa tct gct att      240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65                  70                  75                  80

aaa gaa ttt gga aag tta gat gtt atg att aat aac gca gga atg gaa      288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
                 85                  90                  95

aat ccg gtt tca tct cat gaa atg tct tta agc gat tgg aat aaa gta      336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
            100                 105                 110

att gat acg aac tta acg gga gca ttt tta gga agc cgt gaa gcg att      384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gtg gaa aat gat att aag gga aca gtt att aat atg tcg      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
    130                 135                 140

agt gtt cat gag aaa att cct tgg cca tta ttt gtt cat tac gca gca      480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggt ggc atg aag ctc atg act gaa aca ctt gca tta gaa tat      528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gct cca aaa ggt att cgt gta aat aac att ggg ccg gga gcg att aat      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

aca ccg att aac gct gag aaa ttt gct gat cct aag cag cgc gca gat      624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tac atc gga gag ccg gaa gaa att      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gca gcg gtt gct gca tgg cta gct tct tca gaa gca agt tat gta aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggg att acg ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
```

```
caa gca gga cgc gga taa                                                 786
Gln Ala Gly Arg Gly  *
            260
```

<210> 12
<211> 261
<212> PRT
<213> Bacillus sp.

<400> 12

```
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1               5                  10                  15
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
            20                  25                  30
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
        35                  40                  45
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
    50                  55                  60
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
                85                  90                  95
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
            100                 105                 110
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Arg Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
```

<210> 13
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH.1

<221> CDS
<222> (1)...(765)

<400> 13

```
atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta ggg gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
```

```
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 14
<211> 254
<212> PRT
<213> Agrobacterium sp.

<400> 14

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 15
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH.2

<221> CDS
<222> (1)...(765)

<400> 15

```
atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt caa gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta ggg gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga tta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
```

```
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250


<210> 16
<211> 254
<212> PRT
<213> Agrobacterium sp.

<400> 16
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250

<210> 17
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
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<223> HHDH.16

<221> CDS
<222> (1)...(765)

<400> 17

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
```

```
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 18
<211> 254
<212> PRT
<213> Agrobacterium sp.

<400> 18

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 19
gaattcgccc atatgtatcc ggatttaaaa gg 32

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 20
tggccggatc ctcattaacc gcggcctgcc tgga 34

<210> 21
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 21
gaattcgccc atatgtataa agatttagaa gg 32

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 22
ggccggatcc tcattatccg cgtcctgctt gga 33

<210> 23
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016013-B-03

<221> CDS
<222> (1)...(765)

<400> 23
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1 5 10 15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96

```
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
          20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aaa gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
```

245 250

<210> 24
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016013-B-03

<400> 24
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
1 5 10 15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
20 25 30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
35 40 45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
50 55 60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65 70 75 80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
85 90 95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
100 105 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
115 120 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
130 135 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145 150 155 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
165 170 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
180 185 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
195 200 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
210 215 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225 230 235 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
245 250

<210> 25
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016015-C-04

<221> CDS
<222> (1)...(765)

<400> 25

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct ctg gcg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
```

```
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250


<210> 26
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016015-C-04

<400> 26
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Ala
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250


<210> 27
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016014-E-01
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<221> CDS
<222> (1)...(765)

<400> 27

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gac ctg att gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gac     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aaa cga aag tcg ggg cac atc atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act     432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg     480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat     528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg     576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta     624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
```

```
caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc att ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 28
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016014-E-01

<400> 28

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 29
<211> 768

<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016014-G-08

<221> CDS
<222> (1)...(765)

<400> 29

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg aaa ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

ggt agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa gcc tac      144
Gly Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Ala Tyr
         35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
     50                  55                  60

gct gtc acc agc gct ttt ggt cat gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly His Val Asp Val Leu Val Ser Asn Asp
 65                  70                  75                  80

atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat      288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct cca caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Pro Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg      480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg ttc tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Phe Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
```

```
aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc gct ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Ala Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250

tga                                                                  768
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<210> 30
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016014-G-08

<400> 30

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Gly Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Ala Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly His Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Pro Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Phe Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
```

```
225                 230                 235                 240
Gly Gly Phe Pro Ala Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 31
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH Mz1/2G5

<221> CDS
<222> (1)...(765)

<400> 31

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
```

```
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 32
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH Mz1/2G5

<400> 32

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
```

```
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 33
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH Mz1.1A5

<221> CDS
<222> (1)...(765)

<400> 33

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atg agc ccc gct atc gtc act aac gtc aaa cat ttt ggt ggt atg ggt      48
Met Ser Pro Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

acc gct ctg agg ctg agc gaa gct ggt caa acc gtc gct tgc cat gat      96
Thr Ala Leu Arg Leu Ser Glu Ala Gly Gln Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act     432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
```

```
tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 34
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH Mz1.1A5

<400> 34

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Met Ser Pro Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Thr Ala Leu Arg Leu Ser Glu Ala Gly Gln Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
```

```
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 35
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH cys1.10

<221> CDS
<222> (1)...(765)

<400> 35

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
```

```
ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 36
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH cys1.10

<400> 36

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
```

```
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 37
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH cys2.12

<221> CDS
<222> (1)...(765)

<400> 37

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct gcg cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
```

```
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 38
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH cys2.12

<400> 38

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Ala His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
```

```
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 39
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh133c

<221> CDS
<222> (1)...(852)

<400> 39

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atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat     240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg     288
```

```
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga                  855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 40
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh133c

<400> 40
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1   5   10   15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20   25   30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35   40   45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50   55   60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65   70   75   80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85   90   95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100   105   110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115   120   125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130   135   140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145   150   155   160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165   170   175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180   185   190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195   200   205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210   215   220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225   230   235   240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245   250   255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260   265   270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275   280

<210> 41
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh215

<221> CDS
<222> (1)...(855)

<400> 41
atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct   48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1   5   10   15

```
cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat     240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg     288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac     336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc     384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg att gac gtc gac ctg     432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa     480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc ata aag ggc gcc ttg att ttt acg gct tcc     528
Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
                165                 170                 175

gtg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat     576
Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa     624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat     672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg     720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt     768
```

```
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga                  855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *   *
        275                 280


<210> 42
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh215

<400> 42
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
                165                 170                 175
Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 43
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh267

<221> CDS
<222> (1)...(855)

<400> 43
```
atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aag cat ttt gac cag gtg att gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ctt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Leu Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
```

```
acg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat      576
Thr Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa tga                  855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *   *
        275                 280
```

<210> 44
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh267

<400> 44

```
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Leu Arg Glu
```

```
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Thr Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 45
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh287

<221> CDS
<222> (1)...(855)

<400> 45

```
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
```

```
att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga                  855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *   *
        275                 280
```

<210> 46
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh287

<400> 46

```
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
```

```
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 47
<211> 855
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh320

<221> CDS
<222> (1)...(855)

<400> 47

```
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
             20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
```

```
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
     50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt tat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Tyr Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
```

```
gat atc att gtg gac ggc ggc tac acg ctg ccg taa tga                    855
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *   *
        275                 280


<210> 48
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh320

<400> 48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Tyr Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280

<210> 49
<211> 852
<212> DNA
<213> Artificial Sequence
```

<220>
<223> KRED krh326

<221> CDS
<222> (1)...(852)

<400> 49

```
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat     240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg     288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac     336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc     384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg     432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa     480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc     528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat     576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cac ttc gca aag tcc ctg gcc gtg gaa     624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
```

```
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 50
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh326

<400> 50

```
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
```

```
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280

<210> 51
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh408

<221> CDS
<222> (1)...(852)

<400> 51
atg gct aaa aac ttt agc aat gtc gaa tac cct gcc ccg ccg cca gct      48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac      96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg     144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gct ggc gca gac gtt gcg atc tgg tat     192
Leu Ala Glu Ala Phe Ala Gln Ala Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat     240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg     288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac     336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc     384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg     432
```

```
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt tcc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Ser Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aac      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280


<210> 52
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh408

<400> 52
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Ala Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
```

```
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Ser Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 53
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh417

<221> CDS
<222> (1)...(852)

<400> 53

```
atg gct aaa aac ttt agc aat gtc gaa tat cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
             20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
         35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
     50                  55                  60
```

```
aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtc cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 54
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh417

<400> 54
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1   5   10   15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20   25   30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35   40   45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50   55   60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65   70   75   80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85   90   95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100   105   110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115   120   125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130   135   140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145   150   155   160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165   170   175
Met Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180   185   190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195   200   205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210   215   220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225   230   235   240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245   250   255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260   265   270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275   280

<210> 55
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh483

<221> CDS
<222> (1)...(852)

<400> 55

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
```

```
acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280


<210> 56
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh483

<400> 56
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
```

```
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 57
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh476

<221> CDS
<222> (1)...(852)

<400> 57

```
atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gcg aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
```

```
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtt ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 58
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED krh476

<400> 58

```
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
```

```
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 59
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED krh495

<221> CDS
<222> (1)...(852)

<400> 59

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg ccg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1               5                  10                  15

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc agc tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gcc ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cag gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
```

```
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

att gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg att gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat tat cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc ata aag ggc gcc ttg att ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
                165                 170                 175

gtg tcg ggt cac atc gtt aac att ccg caa ttt cag gcg acc tac aat      576
Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gcc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggt cgt ggt ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gat ggc ggc tac acg ctg ccg taa                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 60
<211> 283
<212> PRT
<213> Artificial Sequence

<220>

<223> KRED krh495

<400> 60
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1   5   10   15
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20   25   30
Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
        35   40   45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50   55   60
Asn Ser Gln Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65   70   75   80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85   90   95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100   105   110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115   120   125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Ile Asp Val Asp Leu
    130   135   140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Tyr Arg Glu
145   150   155   160
Arg Phe Glu Lys Glu Gly Ile Lys Gly Ala Leu Ile Phe Thr Ala Ser
                165   170   175
Val Ser Gly His Ile Val Asn Ile Pro Gln Phe Gln Ala Thr Tyr Asn
            180   185   190
Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195   200   205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210   215   220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225   230   235   240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245   250   255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260   265   270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275   280

<210> 61
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH 2313

<221> CDS
<222> (1)...(789)

<400> 61
atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct   48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1   5   10   15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca   96

```
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta      144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga      192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att      240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg acg atc aat gct gag aaa ttt gct gac cct aaa cag aaa gct gat      624
Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
```

```
                245                 250                 255

cag gca ggc cgc ggt taa tga                                         789
Gln Ala Gly Arg Gly  *   *
            260


<210> 62
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH 2313

<400> 62
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Thr Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260

<210> 63
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
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<223> GDH 2331

<221> CDS
<222> (1)...(789)

<400> 63
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atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct      48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca      96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta     144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga     192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att     240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa     288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc     336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att     384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc     432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca     480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac     528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac     576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat     624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
```

```
gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc gtc acg tta ttc gcg gac ggc ggt atg aca cta tat cct tca ttc      768
Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Leu Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa tga                                        789
Gln Ala Gly Arg Gly  *   *
            260
```

<210> 64
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH 2331

<400> 64

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
```

```
Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Leu Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
```

<210> 65
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH 2279

<221> CDS
<222> (1)...(789)

<400> 65

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atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct       48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca       96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
             20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta      144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
         35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga      192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
     50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att      240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                 85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
```

```
agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat      624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205

gcc gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc gtc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa tga                                         789
Gln Ala Gly Arg Gly  *   *
            260
```

<210> 66
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH 2279

<400> 66

```
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
```

```
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
Ala Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Val Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
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<210> 67
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH 2379

<221> CDS
<222> (1)...(789)

<400> 67

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atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct      48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca      96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
             20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta     144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
         35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga     192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
     50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att     240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa     288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                 85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc     336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att     384
```

```
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc     432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac tat gcg gca     480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg ctt aag ctg atg aca gaa aca tta gcg ttg gaa tac     528
Ser Lys Gly Gly Leu Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac     576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag aaa gct gat     624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc     672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca     720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc     768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa tga                                        789
Gln Ala Gly Arg Gly  *   *
            260
```

<210> 68
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH 2379

<400> 68

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
```

```
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Leu Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
```

<210> 69
<211> 1206
<212> DNA
<213> Artificial Sequence

<220>
<223> FDH FDHPs3

<221> CDS
<222> (1)...(1206)

<400> 69

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atg gca aaa gtt cta tgt gtt cta tat gat gat ccg gtt gat ggt tat       48
Met Ala Lys Val Leu Cys Val Leu Tyr Asp Asp Pro Val Asp Gly Tyr
 1               5                  10                  15

ccg aaa acc tat gca cgt gat gat cta ccg aaa att gat cat tat ccg       96
Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro
            20                  25                  30

ggt ggt cag acc cta ccg acc ccg aaa gca att gat ttt acc ccg ggt      144
Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly
        35                  40                  45

cag cta cta ggt agc gtt agc ggt gaa cta ggt cta cgt aaa tat cta      192
Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu
    50                  55                  60

gaa agc aac ggt cat acc cta gtt gtt acc agc gat aag gac ggc cct      240
Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro
```

```
 65                  70                  75                  80

gac agc gtg ttc gag cgc gag cta gtg gac gcc gac gtg gtg att agc      288
Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser
                85                  90                  95

cag cct ttc tgg cct gcc tat cta acc cct gag cgc att gcc aag gcc      336
Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala
            100                 105                 110

aag aat cta aag cta gcc cta acc gcc ggc att ggc agc gac cat gtg      384
Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val
        115                 120                 125

gac cta cag agc gcc att gac cgc aat gtg acc gtg gcc gag gtg acc      432
Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr
    130                 135                 140

tat tgt aat agc att agc gtg gcc gag cat gtg gtg atg atg att cta      480
Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu
145                 150                 155                 160

agc cta gtg cgc aat tat cta cct tcc cat gaa tgg gcg cgt aaa ggc      528
Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly
                165                 170                 175

ggc tgg aac atc gcg gat tgc gtc tcc cat gcg tat gat ctg gaa gcg      576
Gly Trp Asn Ile Ala Asp Cys Val Ser His Ala Tyr Asp Leu Glu Ala
            180                 185                 190

atg cat gtc ggc acg gtc gcg gcg ggc cgt atc gcc ctg gcg gtc ctg      624
Met His Val Gly Thr Val Ala Ala Gly Arg Ile Ala Leu Ala Val Leu
        195                 200                 205

cgt cgt ctg gcg ccg ttt gat gtc cat ctg cat tat acg gat cgt cat      672
Arg Arg Leu Ala Pro Phe Asp Val His Leu His Tyr Thr Asp Arg His
    210                 215                 220

cgt ctg ccg gaa tcg gta gaa aaa gaa tta aac tta acg tgg cat gcg      720
Arg Leu Pro Glu Ser Val Glu Lys Glu Leu Asn Leu Thr Trp His Ala
225                 230                 235                 240

acg agg gaa gat atg tac cca gta tgt gat gta gta acg tta aac tgt      768
Thr Arg Glu Asp Met Tyr Pro Val Cys Asp Val Val Thr Leu Asn Cys
                245                 250                 255

cca tta cat cca gaa acg gaa cat atg att aac gat gaa acg tta aaa      816
Pro Leu His Pro Glu Thr Glu His Met Ile Asn Asp Glu Thr Leu Lys
            260                 265                 270

tta ttc aaa agg gga gcg tac att gtc aac acg gcg aga ggc aaa ttg      864
Leu Phe Lys Arg Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Lys Leu
        275                 280                 285

tgc gat aga gat gcg gtc gcg aga gcg ttg gaa tca ggc aga ttg gca      912
Cys Asp Arg Asp Ala Val Ala Arg Ala Leu Glu Ser Gly Arg Leu Ala
    290                 295                 300
```

```
ggc tat gcg ggc gat gtc tgg ttt ccg caa ccg gcg ccg aaa gat cat      960
Gly Tyr Ala Gly Asp Val Trp Phe Pro Gln Pro Ala Pro Lys Asp His
305                 310                 315                 320

ccg tgg aga acg atg ccg tat aac ggc atg acg ccg cat att tca ggc     1008
Pro Trp Arg Thr Met Pro Tyr Asn Gly Met Thr Pro His Ile Ser Gly
                325                 330                 335

acg acg ttg acg gcg caa gcg aga tat gct gcg ggc acg aga gaa att     1056
Thr Thr Leu Thr Ala Gln Ala Arg Tyr Ala Ala Gly Thr Arg Glu Ile
            340                 345                 350

ttg gaa tgc ttt ttt gaa ggc aga cca atc cgt gac gaa tat ctg atc     1104
Leu Glu Cys Phe Phe Glu Gly Arg Pro Ile Arg Asp Glu Tyr Leu Ile
        355                 360                 365

gtc cag ggt ggt gcc ctg gcc ggt acc ggt gcc cat tct tat tct aaa     1152
Val Gln Gly Gly Ala Leu Ala Gly Thr Gly Ala His Ser Tyr Ser Lys
    370                 375                 380

ggt aat gcc acc ggt ggt tct gaa gaa gcc aaa ttc aaa aaa gcc gtc     1200
Gly Asn Ala Thr Gly Gly Ser Glu Glu Ala Lys Phe Lys Lys Ala Val
385                 390                 395                 400

taa tga                                                            1206
 *   *
```

<210> 70
<211> 400
<212> PRT
<213> Pseudomonas sp. strain 101

<400> 70

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Met Ala Lys Val Leu Cys Val Leu Tyr Asp Asp Pro Val Asp Gly Tyr
 1               5                  10                  15
Pro Lys Thr Tyr Ala Arg Asp Asp Leu Pro Lys Ile Asp His Tyr Pro
            20                  25                  30
Gly Gly Gln Thr Leu Pro Thr Pro Lys Ala Ile Asp Phe Thr Pro Gly
        35                  40                  45
Gln Leu Leu Gly Ser Val Ser Gly Glu Leu Gly Leu Arg Lys Tyr Leu
    50                  55                  60
Glu Ser Asn Gly His Thr Leu Val Val Thr Ser Asp Lys Asp Gly Pro
65                  70                  75                  80
Asp Ser Val Phe Glu Arg Glu Leu Val Asp Ala Asp Val Val Ile Ser
                85                  90                  95
Gln Pro Phe Trp Pro Ala Tyr Leu Thr Pro Glu Arg Ile Ala Lys Ala
            100                 105                 110
Lys Asn Leu Lys Leu Ala Leu Thr Ala Gly Ile Gly Ser Asp His Val
        115                 120                 125
Asp Leu Gln Ser Ala Ile Asp Arg Asn Val Thr Val Ala Glu Val Thr
    130                 135                 140
Tyr Cys Asn Ser Ile Ser Val Ala Glu His Val Val Met Met Ile Leu
145                 150                 155                 160
Ser Leu Val Arg Asn Tyr Leu Pro Ser His Glu Trp Ala Arg Lys Gly
```

```
                165                 170                 175
Gly Trp Asn Ile Ala Asp Cys Val Ser His Ala Tyr Asp Leu Glu Ala
            180                 185                 190
Met His Val Gly Thr Val Ala Ala Gly Arg Ile Ala Leu Ala Val Leu
        195                 200                 205
Arg Arg Leu Ala Pro Phe Asp Val His Leu His Tyr Thr Asp Arg His
    210                 215                 220
Arg Leu Pro Glu Ser Val Glu Lys Glu Leu Asn Leu Thr Trp His Ala
225                 230                 235                 240
Thr Arg Glu Asp Met Tyr Pro Val Cys Asp Val Val Thr Leu Asn Cys
                245                 250                 255
Pro Leu His Pro Glu Thr Glu His Met Ile Asn Asp Glu Thr Leu Lys
            260                 265                 270
Leu Phe Lys Arg Gly Ala Tyr Ile Val Asn Thr Ala Arg Gly Lys Leu
        275                 280                 285
Cys Asp Arg Asp Ala Val Ala Arg Ala Leu Glu Ser Gly Arg Leu Ala
    290                 295                 300
Gly Tyr Ala Gly Asp Val Trp Phe Pro Gln Pro Ala Pro Lys Asp His
305                 310                 315                 320
Pro Trp Arg Thr Met Pro Tyr Asn Gly Met Thr Pro His Ile Ser Gly
                325                 330                 335
Thr Thr Leu Thr Ala Gln Ala Arg Tyr Ala Ala Gly Thr Arg Glu Ile
            340                 345                 350
Leu Glu Cys Phe Phe Glu Gly Arg Pro Ile Arg Asp Glu Tyr Leu Ile
        355                 360                 365
Val Gln Gly Gly Ala Leu Ala Gly Thr Gly Ala His Ser Tyr Ser Lys
    370                 375                 380
Gly Asn Ala Thr Gly Gly Ser Glu Glu Ala Lys Phe Lys Lys Ala Val
385                 390                 395                 400
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<210> 71
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> FDH FDHCb13

<221> CDS
<222> (1)...(1098)

<400> 71

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atg aaa atc gta ctc gta ctc tac gat gca ggc aaa cac gca gca gat      48
Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
 1               5                  10                  15

gaa gaa aaa ctc tac ggc tgc acg gaa aat aag ctg ggc att gca aat      96
Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala Asn
            20                  25                  30

tgg ctg aag gat cag ggc cac gaa ctg att acg acg tca gat aag gaa     144
Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
        35                  40                  45

ggc ggt aat tcc gtc ttg gat caa cac atc ccc gat gct gat atc atc     192
Gly Gly Asn Ser Val Leu Asp Gln His Ile Pro Asp Ala Asp Ile Ile
    50                  55                  60
```

```
atc aca aca ccc ttc cac ccc gct tac atc aca aaa gaa aga atc gat      240
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp
 65                  70                  75                  80

aaa gct aaa aaa ttg aaa ttg gtc gtc gtc gct ggt gtc ggt tcc gat      288
Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
                85                  90                  95

cac atc gat ttg gat tac atc aat caa aca ggt aaa aaa atc tcc gtc      336
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
            100                 105                 110

ttg gaa gtc aca ggt tcc aat gtc gtc tcc gtc gct gaa cac gtc gtc      384
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
        115                 120                 125

atg aca atg ttg gtc ttg gtc aga aat ttc gtc ccc gct cac gaa caa      432
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
    130                 135                 140

atc atc aat cac gat tgg gaa gtc gct gct atc gct aaa gat gct tac      480
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145                 150                 155                 160

gat atc gaa ggt aaa aca atc gct aca atc ggt gct ggt aga atc ggt      528
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
                165                 170                 175

tac aga gtc ttg gaa aga ttg gtc ccc ttc aat ccc aaa gaa ttg ttg      576
Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu
            180                 185                 190

tac tac gat tac caa gct ttg ccc aaa gat gct gaa gaa aaa gtt ggt      624
Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly
        195                 200                 205

gct cgt cgt gtt gaa aac ata gaa gaa ttg gtt gct cag gct gat ata      672
Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
    210                 215                 220

gtt acc gtt aac gct ccg ttg cac gct ggt acc aaa ggt ttg ata aac      720
Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
225                 230                 235                 240

aaa gaa ttg ttg tca aaa ttt aaa aaa ggt gct tgg ttg ctt aac acc      768
Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Leu Asn Thr
                245                 250                 255

gct cgt ggt gct ata tgc gtt gct gaa gat gtt gct gct gct ttg gaa      816
Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu Glu
            260                 265                 270

tca ggt cag ttg cgt ggt tac ggt ggt gat gtt tgg ttt ccg cag ccg      864
Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
        275                 280                 285
```

```
gct ccg aaa gat cac ccg tgg cgt gat atg cgt aac aaa tac ggt gct      912
Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
    290                 295                 300

ggt aac gct atg acc ccg cac tac tca ggt acc acc ttg gat gct cag      960
Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
305                 310                 315                 320

acc cgt tac gct cag ggt acc aaa aac atc ctc gaa tcg ttt ttt acc     1008
Thr Arg Tyr Ala Gln Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
                325                 330                 335

ggt aaa ttt gat tat cgt cca cag gat atc atc ctc ctc aac ggt gaa     1056
Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
            340                 345                 350

tat gtt acc aaa gcc tat ggt aaa cac gat aaa aaa taa tga             1098
Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys  *   *
        355                 360
```

<210> 72
<211> 364
<212> PRT
<213> Candida boidinii

<400> 72

```
Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
 1               5                  10                  15
Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala Asn
            20                  25                  30
Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
        35                  40                  45
Gly Gly Asn Ser Val Leu Asp Gln His Ile Pro Asp Ala Asp Ile Ile
    50                  55                  60
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Ile Asp
65                  70                  75                  80
Lys Ala Lys Lys Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
                85                  90                  95
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
            100                 105                 110
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
        115                 120                 125
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
    130                 135                 140
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
145                 150                 155                 160
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
                165                 170                 175
Tyr Arg Val Leu Glu Arg Leu Val Pro Phe Asn Pro Lys Glu Leu Leu
            180                 185                 190
Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Asp Ala Glu Glu Lys Val Gly
        195                 200                 205
Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
    210                 215                 220
Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
225                 230                 235                 240
```

```
Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Leu Asn Thr
                245                 250                 255
Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu Glu
            260                 265                 270
Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
        275                 280                 285
Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
    290                 295                 300
Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
305                 310                 315                 320
Thr Arg Tyr Ala Gln Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
                325                 330                 335
Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
            340                 345                 350
Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
        355                 360
```

<210> 73
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016514-B-12

<221> CDS
<222> (1)...(765)

<400> 73

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
```

```
aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 74
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016514-B-12

<400> 74

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
```

```
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 75
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH Mz1/4H6

<221> CDS
<222> (1)...(765)

<400> 75

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt ggt ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
```

```
tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg ccg tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 76
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH Mz1/4H6

<400> 76

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
```

```
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 77
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016229-F-04

<221> CDS
<222> (1)...(765)

<400> 77

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agt gct ctg agg ctg tcg gag gct ggt cac acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gag gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gga ctg att gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
```

```
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 78
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016229-F-04

<400> 78
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly

```
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Gly Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 79
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016230-A-08

<221> CDS
<222> (1)...(765)

<400> 79

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
             20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
         35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
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Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
     50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tat cgt ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gaa cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 80
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016230-A-08

<400> 80
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35   40   45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50   55   60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65   70   75   80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85   90   95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100   105   110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115   120   125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130   135   140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145   150   155   160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165   170   175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180   185   190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195   200   205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210   215   220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225   230   235   240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245   250

<210> 81
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016096-G9

<221> CDS
<222> (1)...(765)

<400> 81
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt 48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat 96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30

```
gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc att atc gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 82
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016096-G9

<400> 82
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35   40   45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50   55   60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65   70   75   80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85   90   95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100   105   110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115   120   125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130   135   140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145   150   155   160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165   170   175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180   185   190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195   200   205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210   215   220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225   230   235   240
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu
                245   250

<210> 83
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016097-F9

<221> CDS
<222> (1)...(765)

<400> 83
atg acc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt   48
Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
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ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250


<210> 84
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016097-F9

<400> 84
Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250


<210> 85
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016097-H10

<221> CDS
<222> (1)...(765)
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<400> 85

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Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act     432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg     480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat     528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg     576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta     624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg     672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
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```
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 86
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016097-H10

<400> 86

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Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 87
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016099-A1

<221> CDS
<222> (1)...(765)

<400> 87
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Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
         35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
     50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat atc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp
 65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc cag gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
```

```
       195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 88
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016099-A1

<400> 88

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Met Thr Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Ile Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Gln Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 89
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016231-A-03

<221> CDS
<222> (1)...(765)

<400> 89
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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct tca gaa ttt cag cca atc gat aaa tac gcc gtc gaa gat      288
Ile Phe Ala Ser Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tat cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
```

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Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250


<210> 90
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016231-A-03

<400> 90
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Ser Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
```

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Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250

<210> 91
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH P016231-E-03

<221> CDS
<222> (1)...(765)

<400> 91
atg agc acc gct atc gtc acc aac gtc aag cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat     288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aag gag cta tcg act     432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg     480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
```

```
aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac tat tat ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 92
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH P016231-E-03

<400> 92

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
```

```
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 93
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S00827801

<221> CDS
<222> (1)...(765)

<400> 93

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa ggt ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Gly Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
```

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tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 94
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00827801

<400> 94

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Gly Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
```

```
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 95
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S00890554

<221> CDS
<222> (1)...(765)

<400> 95

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cta gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
```

```
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc acg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 96
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00890554

<400> 96

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
```

```
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 97
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S00994580

<221> CDS
<222> (1)...(765)

<400> 97

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atg agc acc gct att gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cta gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
```

```
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc acg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250


<210> 98
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00994580

<400> 98
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
```

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Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Thr Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 99
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S01018044

<221> CDS
<222> (1)...(765)

<400> 99

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat     240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
```

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atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat      288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                 85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg      480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 100
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S0108044

<400> 100

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
```

```
            20                  25                  30
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
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<210> 101
<211> 765
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S01035939

<221> CDS
<222> (1)...(765)

<400> 101

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atg agc acc gct att gtc acc aac gtc aaa cat ttt gga ggt atg ggt      48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat      96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac     144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg att gaa     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
```

```
gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65                  70                  75                  80

atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat      288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg      480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
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<210> 102
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S01035939

<400> 102
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35   40   45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50   55   60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65   70   75   80
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85   90   95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100   105   110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115   120   125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130   135   140
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145   150   155   160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165   170   175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180   185   190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195   200   205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210   215   220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225   230   235   240
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
                245   250

<210> 103
<211> 768
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S01009684

<221> CDS
<222> (1)...(765)

<400> 103
atg agc act gcg att gtt act aac gtc aaa cat ttc ggt ggt atg ggg 48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15

agt gcg ctg aaa ctg tcg gag gcc ggt cat aca gta gcg tgt cac gat 96
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30

gaa agt ttc aaa caa aag gac gaa ttg gaa gcc ttt gcg gaa act tac 144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr

```
        35                  40                  45

cca cag ctg aaa ccg atg tca gaa cag gag cca gcg gag tta att gag     192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
     50                  55                  60

gcg gtc acc agt gcc ttc ggc cag gtg gat gtc ctg gtt agc aac gac     240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
 65                  70                  75                  80

atc ttt gct ctg gaa ttc cag ccg att gac aag tat gcc gtc gaa gac     288
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                 85                  90                  95

tac cgt ggt gcg gta gaa gca ctg cag atc aag ccg ttc gcg ttg gtt     336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Lys Pro Phe Ala Leu Val
            100                 105                 110

aat gcc gta gct agt caa atg aaa aaa cgt aaa tca ggt cat att atc     384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc att act agc gcg gct ccg ttt ggt cca tgg aag gag ctg tcg act     432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tat agt agt gcg cgc gcc ggg gcc tcc gcg ttg gct aac gca ctg agt     480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aaa gaa tta ggt gag tat aat atc cct gtt ttc gcc att ggg cca aac     528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tat ctg cac tca gaa gat agc cca tac tat tac cca acg gaa ccg tgg     576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag atc aac cct gaa cat gtg gcg cat gtt aaa aaa gta aca gcc tta     624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cgt ctg ggt act caa aaa gaa ctt ggc gag ctg gtt gcg ttt ctc     672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gct tct ggt agc tgc gat tac ttg acc ggc caa gtc ttc tgg tta gcc     720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggt ggc ttt ccg gtg att gag cgc tgg cca ggt atg ccg gaa taa         765
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250

tga                                                                 768

<210> 104
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<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S01009684

<400> 104
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15
Ser Ala Leu Lys Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20   25   30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35   40   45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50   55   60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65   70   75   80
Ile Phe Ala Leu Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85   90   95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Lys Pro Phe Ala Leu Val
            100   105   110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115   120   125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130   135   140
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145   150   155   160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165   170   175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180   185   190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195   200   205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210   215   220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225   230   235   240
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
                245   250

<210> 105
<211> 774
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S00817219

<221> CDS
<222> (1)...(765)

<400> 105
atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt   48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1   5   10   15

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agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gct ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt tcc cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
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Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250

tgaggatcc                                                          774

<210> 106
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00817219

<400> 106
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Ser Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250

<210> 107
<211> 774
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S00708827

<221> CDS
<222> (1)...(765)
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<400> 107

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gac ctg att gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct tac ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aaa cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct act ccg ttc ggg cca tgg aaa gag cta tcg act      432
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct tgt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttc ctg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
```

```
gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc ata ata gaa cgt tgg ccc ggc atg ccc gaa taa        765
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250

tgaggatcc                                                          774

<210> 108
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00708827

<400> 108
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Asp Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Tyr Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Thr Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Cys Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Ile Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250

<210> 109
<211> 765
<212> DNA
<213> Artificial Sequence
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<220>
<223> HHDH S00772501

<221> CDS
<222> (1)...(765)

<400> 109

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aaa cag aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cca gaa ttt cag cca atc gat aaa tac gct gtc gaa gat      288
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac act tcg gct cga gct ggg gct agt act cta gct aat gct cta tcg      480
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175

tac cta cac tcg gag gat tcg ccg tac ttc tac ccg act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag act aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
```

```
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc atg ata gaa cgt tgg ccc ggc atg ccc gaa taa          765
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu  *
                245                 250
```

<210> 110
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S00772501

<400> 110

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Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys Gln Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Pro Glu Phe Gln Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Thr Ser Ala Arg Ala Gly Ala Ser Thr Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Phe Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Thr Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Met Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 111
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> HHDH S01035968

<221> CDS
<222> (1)...(765)

<400> 111

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atg agc acc gct atc gtc acc aac gtc aaa cat ttt gga ggt atg ggt       48
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15

agc gct ctg agg ctg agc gaa gct ggt cat acc gtc gct tgc cat gat       96
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30

gaa agc ttt aag cat aaa gat gaa ctg gaa gct ttt gct gaa acc tac      144
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45

cca cag ctg aaa cca atg agc gaa cag gaa cca gct gaa ctg atc gaa      192
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60

gct gtc acc agc gct ttt ggt cag gtc gat gtc ctg gtc agc aac gat      240
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80

atc ttt gct cta gaa ttt cgg cca atc gat aaa tac gct gtc gag gat      288
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95

tac agg ggt gct gtc gaa gct ctg cag atc agg cca ttt gct cta gtg      336
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110

aat gct gtg gct tcg caa atg aag aag cga aag tcg ggg cac atc atc      384
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125

ttc atc act tcg gct gcc ccg ttc ggg cca tgg aag gag cta tcg act      432
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140

tac tct tcg gct cga gct ggg gct agt gca cta gct aat gct cta tcg      480
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160

aag gag cta gga gag tac aat atc ccg gtg ttc gct atc ggg ccg aat      528
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
```

```
tac cta cac tcg gag gat tcg ccg tac tat tac ccc act gag ccg tgg      576
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190

aag att aat ccg gag cac gtg gct cac gtg aag aag gtg act gct cta      624
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205

caa cga cta ggg act caa aaa gag ttg ggg gaa ttg gtg gca ttt ttg      672
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
    210                 215                 220

gca tct ggc tct tgt gat tat ttg act ggc cag gtg ttt tgg ttg gca      720
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240

ggc ggc ttt ccc gtc ata gaa cgt tgg ccc ggc atg ccc gaa              762
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 112
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> HHDH S01035968

<400> 112

```
Met Ser Thr Ala Ile Val Thr Asn Val Lys His Phe Gly Gly Met Gly
 1               5                  10                  15
Ser Ala Leu Arg Leu Ser Glu Ala Gly His Thr Val Ala Cys His Asp
            20                  25                  30
Glu Ser Phe Lys His Lys Asp Glu Leu Glu Ala Phe Ala Glu Thr Tyr
        35                  40                  45
Pro Gln Leu Lys Pro Met Ser Glu Gln Glu Pro Ala Glu Leu Ile Glu
    50                  55                  60
Ala Val Thr Ser Ala Phe Gly Gln Val Asp Val Leu Val Ser Asn Asp
65                  70                  75                  80
Ile Phe Ala Leu Glu Phe Arg Pro Ile Asp Lys Tyr Ala Val Glu Asp
                85                  90                  95
Tyr Arg Gly Ala Val Glu Ala Leu Gln Ile Arg Pro Phe Ala Leu Val
            100                 105                 110
Asn Ala Val Ala Ser Gln Met Lys Lys Arg Lys Ser Gly His Ile Ile
        115                 120                 125
Phe Ile Thr Ser Ala Ala Pro Phe Gly Pro Trp Lys Glu Leu Ser Thr
    130                 135                 140
Tyr Ser Ser Ala Arg Ala Gly Ala Ser Ala Leu Ala Asn Ala Leu Ser
145                 150                 155                 160
Lys Glu Leu Gly Glu Tyr Asn Ile Pro Val Phe Ala Ile Gly Pro Asn
                165                 170                 175
Tyr Leu His Ser Glu Asp Ser Pro Tyr Tyr Tyr Pro Thr Glu Pro Trp
            180                 185                 190
Lys Ile Asn Pro Glu His Val Ala His Val Lys Lys Val Thr Ala Leu
        195                 200                 205
Gln Arg Leu Gly Thr Gln Lys Glu Leu Gly Glu Leu Val Ala Phe Leu
```

```
    210                 215                 220
Ala Ser Gly Ser Cys Asp Tyr Leu Thr Gly Gln Val Phe Trp Leu Ala
225                 230                 235                 240
Gly Gly Phe Pro Val Ile Glu Arg Trp Pro Gly Met Pro Glu
                245                 250
```

<210> 113
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED S01040430

<221> CDS
<222> (1)...(852)

<400> 113

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15

cat acc aaa aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
```

```
cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca cag aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg tag                     852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 114
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED S01040430

<400> 114

```
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
```

```
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 115
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED S01091361

<221> CDS
<222> (1)...(852)

<400> 115

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atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15

cat acc aaa gac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60

aac agt cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
```

```
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gca ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac att gtt aat gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg cag gaa aca caa aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc gtt gtg gac ggc ggc tac acg ctg ccg tag                     852
Asp Ile Val Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 116
<211> 283
<212> PRT
<213> Artificial Sequence

<220>

<223> KRED S01091361

<400> 116
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1   5   10   15
His Thr Lys Asp Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20   25   30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35   40   45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50   55   60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65   70   75   80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85   90   95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100   105   110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115   120   125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130   135   140
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145   150   155   160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165   170   175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180   185   190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195   200   205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210   215   220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225   230   235   240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245   250   255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260   265   270
Asp Ile Val Val Asp Gly Gly Tyr Thr Leu Pro
        275   280

<210> 117
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED S01091625

<221> CDS
<222> (1)...(852)

<400> 117
atg gct aaa aac ttt tcc aat gtc gaa tat cct gcc ccg gcg cca gct 48
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1   5   10   15

cat acc aag aac gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac 96

```
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
         35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
     50                  55                  60

aac agt cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                 85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtg gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gca ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gag aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aat gtg ccg caa ttt cag gcg acc tac aat      576
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gaa aca caa aat aga tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Arg Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
```

```
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc aca      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg tag                      852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280


<210> 118
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED S01091625

<400> 118
Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15
His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Ala Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Arg Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
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<210> 119
<211> 852
<212> DNA
<213> Artificial Sequence

<220>
<223> KRED S01094648

<221> CDS
<222> (1)...(852)

<400> 119
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atg gct aaa aac ttt tcc aat gtc gga tat cct gcc ccg gcg cca gct       48
Met Ala Lys Asn Phe Ser Asn Val Gly Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15

cat acc aaa agc gaa tca ctg cag gta ctg gat ctg ttc aaa ctg aac       96
His Thr Lys Ser Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30

ggc aaa gtc gcg tct atc acc ggt agc aac tca ggc att ggt tac gcg      144
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
         35                  40                  45

ctg gcc gaa gct ttt gcg cag gtt ggc gca gac gtt gcg atc tgg tat      192
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
     50                  55                  60

aac agc cat gat gcc acc ggt aaa gca gag gcc ctg gct aaa aaa tat      240
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
 65                  70                  75                  80

ggc gta aaa gtc aag gct tat aaa gct aat gtc agc tcg agt gat gcg      288
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95

gtg aaa cag act att gag cag cag atc aag gat ttt ggc cac ctg gac      336
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110

ata gtt gtg gcg aac gca ggc atc cca tgg act aag ggt gca tac atc      384
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125

gat cag gat gac gat aaa cat ttt gac cag gtg gtt gac gtc gac ctg      432
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140

aaa ggc gta ggc tat gta gca aaa cat gcg ggt cgc cat ttt cgt gaa      480
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160

cgt ttc gaa aaa gaa ggc aaa aag ggc gcc ttg gtc ttt acg gct tcc      528
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175

atg tcg ggt cac atc gtt aac gtg ccg caa ttt cag gcg gcc tac aat      576
```

```
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
            180                 185                 190

gcg gtc aag gca ggc gtg cgt cat ttc gca aag tcc ctg gcc gtg gaa      624
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205

ttt gct cct ttc gca cgt gtt aac tct gta tct cct ggc tat att aat      672
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220

acc gag atc tct gat ttc gtc ccg caa gga aca cag aat aaa tgg tgg      720
Thr Glu Ile Ser Asp Phe Val Pro Gln Gly Thr Gln Asn Lys Trp Trp
225                 230                 235                 240

agc tta gtt cca ttg ggc cgt ggc ggg gaa act gcg gaa tta gtt ggt      768
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255

gcc tac ctg ttc ctg gca agt gat gcg ggc tcc tac gcc acg ggc acg      816
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270

gat atc att gtg gac ggc ggc tac acg ctg ccg tag                     852
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro  *
        275                 280
```

<210> 120
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRED S01094648

<400> 120

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Met Ala Lys Asn Phe Ser Asn Val Gly Tyr Pro Ala Pro Ala Pro Ala
 1               5                  10                  15
His Thr Lys Ser Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
            20                  25                  30
Gly Lys Val Ala Ser Ile Thr Gly Ser Asn Ser Gly Ile Gly Tyr Ala
        35                  40                  45
Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
    50                  55                  60
Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65                  70                  75                  80
Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
                85                  90                  95
Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
            100                 105                 110
Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
        115                 120                 125
Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
    130                 135                 140
Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145                 150                 155                 160
```

```
Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
                165                 170                 175
Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Ala Tyr Asn
            180                 185                 190
Ala Val Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
        195                 200                 205
Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
    210                 215                 220
Thr Glu Ile Ser Asp Phe Val Pro Gln Gly Thr Gln Asn Lys Trp Trp
225                 230                 235                 240
Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
                245                 250                 255
Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
            260                 265                 270
Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro
        275                 280
```

<210> 121
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH S01024744

<221> CDS
<222> (1)...(789)

<400> 121

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atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct       48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca       96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta      144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga      192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att      240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
```

```
atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat      624
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa tga                                         789
Gln Ala Gly Arg Gly  *   *
            260
```

<210> 122
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH S01024744

<400> 122

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Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
```

```
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260

<210> 123
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH S01052992

<221> CDS
<222> (1)...(789)

<400> 123
atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct gct      48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1               5                  10                  15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca      96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta     144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga     192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att     240
```

```
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggt ggg atg aag ctg atg aca aaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Met Lys Leu Met Thr Lys Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aat      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat      624
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gat gag atc      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Asp Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc tgc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Cys Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

cag gca ggc cgc ggt taa tga                                         789
Gln Ala Gly Arg Gly  *   *
            260
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<210> 124
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH S01052992

<400> 124
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1   5   10   15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20   25   30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35   40   45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50   55   60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65   70   75   80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85   90   95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100   105   110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115   120   125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130   135   140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145   150   155   160
Ser Lys Gly Gly Met Lys Leu Met Thr Lys Thr Leu Ala Leu Glu Tyr
                165   170   175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180   185   190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195   200   205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Asp Glu Ile
    210   215   220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Cys Tyr Val Thr
225   230   235   240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245   250   255
Gln Ala Gly Arg Gly
            260

<210> 125
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> GDH S01063714

<221> CDS
<222> (1)...(789)

<400> 125
atg tat ccg gat tta aaa gga aaa gtc gtc gct att aca gga gct act 48
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Thr
 1   5   10   15

tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag gag cag gca 96
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala

```
            20                  25                  30

aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg aac gag gta      144
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45

aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc gtc caa gga      192
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60

gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa acg gca att      240
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80

aag gag ttc ggc aca ctc gat att atg att aat aat gcc ggt ctt gaa      288
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95

aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg gat aaa gtc      336
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110

atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt gaa gcg att      384
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125

aaa tat ttc gta gaa aac gat atc aag gga aat gtc att aac atg tcc      432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140

agt gtg cac gaa gtg att cct tgg cca tta ttt gtc cac tat gcg gca      480
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc ggg atg aag ctg atg aca gaa aca tta gcg ttg gaa tac      528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt gcg atc aac      576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

acg acg atc aat aag gag aaa ttt gct gac cct gaa cag aga gct gat      624
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tat atc ggc gaa ccg gag gag atc      672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc tac gtc aca      720
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat cct tca ttc      768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
```

```
cag gca ggc cgc ggt taa tga                                              789
Gln Ala Gly Arg Gly  *   *
            260


<210> 126
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> GDH S01063714

<400> 126
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Thr
 1               5                  10                  15
Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
            20                  25                  30
Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
        35                  40                  45
Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
    50                  55                  60
Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65                  70                  75                  80
Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
                85                  90                  95
Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
            100                 105                 110
Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
    130                 135                 140
Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190
Thr Thr Ile Asn Lys Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220
Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225                 230                 235                 240
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255
Gln Ala Gly Arg Gly
            260
```